Abstract

The present invention relates to novel genes located in two chromosomal regions within uropathogenic *E. coli* that are associated with virulence. These chromosomal regions are known as pathogenicity islands (PAIs). In particular, the present application discloses 142 sequenced fragments (contigs) of DNA from two pools of cosmids covering pathogenicity islands PAI IV and PAI V located on the chromosome of the uropathogenic *Escherichia coli* J96. Further disclosed are 351 predicted protein-coding open reading frames within the sequenced fragments.